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Range: from  to  Features: ☒ CDD

☐ **1:** [11360168](#). Reports ...[\[gi:11360168\]](#) This record has been discontinued.

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LOCUS T46372 859 aa linear PRI 04-FEB-2000  
 DEFINITION hypothetical protein DKFZp434P1818.1 - human (fragment).  
 ACCESSION T46372  
 VERSION T46372 GI:11360168  
 DBSOURCE pir: locus T46372;

summary: #length 859 #checksum 5631  
 ;  
 genetic: #note DKFZp434P1818.1  
 ;  
 PIR dates: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 ;  
 punctuation in sequence.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (residues 1 to 859)

AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE Direct Submission

JOURNAL Submitted (??-JAN-2000) to the Protein Sequence Database

COMMENT [WARNING] On Sep 13, 2005 this sequence was replaced by [gi:74719265](#).

FEATURES

source Location/Qualifiers  
 1..859  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 Protein 1..859  
 /product="hypothetical protein DKFZp434P1818.1"  
 Region <5..294  
 /region\_name="COG5329"  
 /note="Phosphoinositide polyphosphatase (Sac family)  
 [Signal transduction mechanisms]; COG5329"  
 /db\_xref="CDD:34909"

ORIGIN

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121 qvllfnnshl tyvsfdfheh crgmkfenvq tltdaiydii ldmkwcwvde agvickqegi
181 frvncmdcld rtnvvqaaia rvvmeqqllk lgvmpeqpl pvkcniyqi mwanngdsis
241 rgyagtaalk gdftrtgerk lagvmkdgvn sanryylnrf kdayrqavid lmqqipvted
301 lysiftkeke healhkenqr shqelisql l qsymkl lllpd dekfhhggwal idcdpslida
  
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361 thrdvdlvll lsnsayyvay yddevdkvnq yqrlslenle kieigpeptl fgkpkfscmr
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481 kphediigir sqnqgsllaqg knflmskfss lnqkvkqtkn nvnlgnlrkl gnftkpemkv
541 nflkpnlkvn lwksdsslet mentgvmdkv qaesdgdmss dndsyhsdef ltnksdeder
601 qlanslesvg pidyvlpscq iiasaprlgs rsqslsstds svhapseitv ahgsglgkgq
661 esplkkspsa gdvhiltgfa kpmdiychrh vqdaqnkvtl lsetrsvsqq asqernqmtl
721 qvsdetqses teqtpsrpsq ldvslsatgp qflsvepahs vasqktptsa ssmleletgl
781 hvtpspsess ssravspfhk irssmvqvas itqagltlthgi nfvskvqks ppepeiinqv
841 qqnelkkmfh qcqtriifi
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//

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